

FOUNDER CONTRIBUTION IN THE ENDANGERED CZECH DRAUGHT HORSE BREEDS ¹

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ABSTRACT

There are many horse breeds included in conservation programs around the world. The current populations of these breeds have often been derived from a small number of founders. The genetic structure of two endangered horse breeds – Silesian Noriker and Czech-Moravian Belgian was studied based on founder contribution analysis. Silesian Norikers are descended from 1235 founders and Czech-Moravian Belgians are descended from 2583 founders. The effective numbers of founders and ancestors contributing to the current genetic pool were 69.42 and 22.32 for the Silesian Noriker breed and 43.33 and 23.32 for the Czech-Moravian Belgian breed respectively. Approximately 50 % of total genetic variation was explained by 31 founders with the greatest influence for the Silesian Noriker and 47 most influential founders for the Czech-Moravian Belgian, with a maximum individual contribution of 8 % for Silesian Noriker and 14 % for Czech-Moravian Belgian. These results suggest that the genetic variability has decreased and without changes in breeding strategy, the genetic variability might continue to decline. The further expected loss of genetic variability in the populations can be minimized by increasing the number of descendants of low-represented founders.

Key words: horses, Czech draught horses, endangered breeds, Silesian Noriker, Czech Moravian Belgian, genetic diversity, founders contributions

1 INTRODUCTION

Domestic animals have been subjected to a great pressure to evolve to meet the changing needs of a commercialized, mechanized and globalized world in the last hundred years. Nowadays a large number of the world's breeds are in a danger of extinction. As happened with breeds of other domestic species, some horse breeds became endangered because they do not appear to meet the current needs of humans.

The Silesian Noriker and Czech-Moravian Belgian draught horse breeds belong to a group of endangered horse breeds recognized as Genetic Resources in the Czech Republic. Over the last 120 years, the Czech-

Moravian Belgian breed was developed in the Czech Republic territory primarily using imported Belgian stallions and, to a lesser extent, Walloons. The Silesian Noriker breed was formed over the last 100 years from imported Noriker stallions and Bavarian draught stallions. World War II had a negative impact on breeding programs because there was a steep decrease in a number of horses. The post-war expansion of farm mechanization caused a further decrease in numbers. The Silesian Noriker and Czech-Moravian Belgian horse were registered as separate breeds until the 1960s, but because of their decreasing numbers, all animals were merged into a single registry, the Draught horse. At this time, stallions and mares were used across the breeds. However,

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in 1989, draught horses in the Czech Republic were re-assigned into the three original populations (Silesian Noriker, Czech-Moravian Belgian and Noriker) based on morphological analysis. After 1996 and 1999 respectively, the populations of Silesian Noriker and Czech-Moravian Belgian horses were certified as rare and endangered breeds (Genetic Resources) and their studbooks were closed. The above mentioned history and the restricted size of the population affected composition of the gene pool of these breeds.

The objective of the present study was to describe a loss of genetic diversity due to unequal level of founder contributions to the reference population in two endangered Czech draught horse breeds.

2 MATERIAL AND METHODS

2.1 DATA

A total of 27,022 pedigree records of individuals registered in studbooks from 1900 to 31st June 2013 were provided from the Association of Horse Breeders Unions of the Czech Republic. Pedigree analyses were performed using two reference populations containing animals potentially contributing to the next generations. The reference populations were defined as the entire active population of individuals (stallions and mares) born in the period from 1996 to 2010 ($n = 498$ for Silesian Noriker and $n = 956$ for Czech-Moravian Belgian horse).

2.2 PEDIGREE COMPLETENESS MEASURES

The pedigree completeness and the number of ancestral generations influence the estimated inbreeding coefficients and the relationship coefficients between animals. The pedigree completeness level (PCL) was assessed as the proportion of ancestors known per generation for each offspring (MacCluer *et al.*, 1983). The number of equivalent complete generations (t) in the pedigree was computed using the formula $\Sigma(1/2)^n$ (Maignel *et al.*, 1996), where n is the number of generations between an animal and its ancestor.

2.3 PROBABILITY OF GENE ORIGIN

Several measures of genetic variability were calculated from the pedigree data. The total number of founders (f) for each breed was determined as the total number of ancestors with unknown parents. The effective number of founders (f_e) is defined as the number of

founders explaining the same level of genetic diversity as that observed in the reference population (Lacy, 1989). This parameter is the reciprocal of the probability that two randomly drawn genes in the population under the study originated from the same founder (James, 1972). The effective number of founders was estimated using the formula:

$$f_e = \frac{1}{\sum_{i=1}^f q_i^2},$$

where q_i is the genetic contribution of the i -th founder to the reference population.

The effective number of ancestors (f_a) is defined as the minimum number of ancestors, not necessarily of founders, explaining the same level of genetic diversity as that observed in the reference population (Boichard *et al.*, 1997). The effective number of ancestors was obtained after determining the marginal genetic contribution of each ancestor. The parameter f_a accounts for losses of genetic variability resulting from bottlenecks caused by unequal contributions among reproductive individuals to future generations. The effective number of ancestors was estimated using the formula:

$$f_a = \frac{1}{\sum_{i=1}^a p_i^2},$$

where p_i is the marginal genetic contribution of ancestor i , and a is the total number of ancestors.

Relatedness coefficient (AR) of a founder individual designates a percentage measure of the extent to which the founder can be regarded as the origin of the reference population.

The founder genome equivalent (f_{ge}) is defined as the effective number of founders with a non-random loss of founder alleles resulting in identical genetic variability to that defined in the reference population (Lacy, 1989). The founder genome equivalent accounts for both unequal contributions of founders and the random loss of alleles caused by genetic drift (Lacy, 1989). The founder genome equivalent was calculated using the method of Caballero and Toro (2000):

$$f_{ge} = \frac{1}{2f_g},$$

where f_g is the average coancestry coefficient for the reference population. According to Caballero and Toro (2000), the average coancestry coefficient was estimated using the formula:

$$f_g = \frac{\sum_{i=1}^n \sum_{j=1}^n a_{ij}}{2n^2},$$

where a_{ij} represents the elements of the relatedness matrix (\mathbf{A}) and n is the number of individuals in the pedigree.

The founder contribution to the reference popula-

tions was calculated as an average relatedness coefficient between founder and individuals in the reference population (Gutiérrez and Goyache, 2005).

2.4 RELATEDNESS COEFFICIENT (AR)

Relatedness coefficient of each pair of individuals was estimated using a tabular method (Falconer and Mackay, 1996), based on VanRaden's method (1992). The average relatedness coefficient of each individual (AR) was computed as the average coefficient integrating the row from the individual in the numerator relationship matrix **A**. This coefficient indicates the probability that a randomly selected allele in the population occurs in a selected individual or amongst a group of individuals (Goyache *et al.*, 2003).

3 RESULTS AND DISCUSSION

The average equivalent of the known generations in the analysed breeds was 8.91, 8.45, and 9.81 for the Czech-Moravian Belgian, Noriker and Silesian Noriker breeds, respectively. Pedigree completeness levels (PCL) were also consistent with the preceding values (Fig. 1). The completeness level declined to less than 50 % after 17, 15, and 14 generations in the SN, CMB and N breeds, respectively.

Compared with the total number of founders, the number of effective founders was low (Table 1). The Silesian Noriker population was based on 1235 founders, while the Czech-Moravian Belgian had 2379 founders,

which represents 4.6 % and 8.8 % of the total pedigree population. The effective number of founders markedly differed among breeds, with 69.49 in the Silesian Noriker and 43.33 in the Czech-Moravian Belgian horse. These values indicate variable genetic contributions from the ancestors. The effective number of founders (f_e) considerably differed from the effective number of ancestors (f_a) for both breeds, suggesting a past bottleneck event. The importance of genetic drift was evaluated based on the ratio of the founder genome equivalent to the effective number of founders and the ratio of the effective number of ancestors to the effective number of founders. The value of each of these ratios was lower than one. The ratios were lower in the Silesian Noriker (0.12 and 0.32) than in the Czech-Moravian Belgian horse (0.25 and 0.53). Particularly, the f_{ge}/f_e ratio suggests that significant genetic drift occurred at some point in the past for each of these breeds. This suggests that the vast majority of founders made a low contribution to the genetic variability of the reference population, which led to a loss of genetic diversity as the result of the unequal contribution of founders (Lacy, 1989). The ratios calculated in the present study had higher or similar values compared with other reports, including the Austrian Noriker – 0.25 and 0.09 (Druml *et al.*, 2009), Lusitano – 0.47 and 0.21 (Vicente *et al.*, 2012) and Spanish Arabian horses – from 0.46 to 0.72 and 0.23 to 0.42 (Cervantes *et al.*, 2008). These values are markedly higher than those reported in other breed included in the gene resources of the Czech Republic, Old Kladruber – 0.27 and 0.05 (Vostrá-Vydrová *et al.*, 2016).

Half of the genetic variation in the reference population of the Czech-Moravian Belgian horse can be ex-

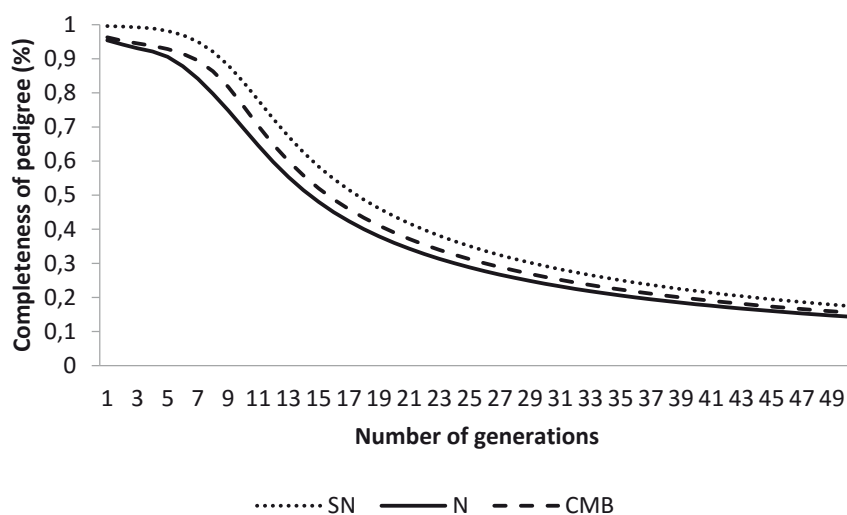


Figure 1: Completeness of pedigree information (PCL) across generations for Silesian Noriker, Noriker and Czech-Moravia Belgian draught horses

Table 1: Parameters characterizing the probability of gene origin

	Silesian Noriker	Czech-Moravian Belgian
Number of animals in the reference population	498	956
Total number of founders (f)	1235	2583
Effective number of founders (f_e)	69.42	43.33
Effective number of ancestors (f_a)	22.32	23.31
Founder genome equivalent (f_{ge})	8.64	11.01

plained by forty seven founders with the most important founder contributing 14 % (Table 2). Four founders contributed 20 % of the gene pool in the reference population. Only thirty one founders are needed to explain 50 % of all genetic diversity in the reference population of the Silesian Noriker and only one founder contributed as much as 8 % of the gene pool (Table 2). Genetic contributions of the Czech-Moravian Belgian founder animals were less balanced. A comparable results were found in the Lipizzan horses where 4.15 % of founders covered 50 % of the pool (Zechner *et al.*, 2002), and for example in the British and Irish Thoroughbred horses, where

6.33 % of founders with the highest contributions were responsible for 45 % of the pool (Cunningham *et al.*, 2001). The significant difference between genealogically important founders was also confirmed by Zechner *et al.* (2002) in their study on Lipizzan horses.

Regarding the breed of Silesian Noriker founder animals, 67 % of gene contributions come from animals of unknown origin, 25 % of gene contributions come from animals imported from Austria (Noriker breed) and 6 % of gene contributions come from local draught horses. In the Czech-Moravian Belgian, 46 % of gene contributions come from animals of unknown origin, 36 % of

Table 2: Genetic contributions of the first twenty founders of the Silesian Noriker and Czech-Moravian Belgian born between 1996 and 2010

Silesian Noriker					Czech-Moravian Belgian				
Individual	Contribution	year*	breed	sex**	Individual	Contribution	year*	breed	sex**
316	0.087	0	unknown	2	316	0.145	0	unknown	2
365	0.044	0	unknown	2	2178	0.018	1917	Belgian draught	1
359	0.039	0	unknown	2	2154	0.017	1916	Belgian draught	1
411	0.033	0	unknown	2	343	0.017	0	unknown	2
1084	0.030	0	unknown	2	2160	0.017	0	Belgian draught	1
407	0.017	0	unknown	2	2239	0.016	0	Belgian draught	1
1620	0.015	0	Czech draught	1	341	0.012	1956	unknown	2
412	0.014	0	unknown	2	349	0.011	0	unknown	2
1704	0.013	0	Czech draught	1	1758	0.011	0	Czech draught	2
689	0.013	0	unknown	2	508	0.010	0	unknown	2
417	0.012	0	unknown	2	829	0.009	0	unknown	2
1877	0.010	0	Noriker	1	2118	0.009	0	Belgian draught	1
1878	0.010	0	Noriker	1	2157	0.009	0	Belgian draught	1
370	0.010	0	unknown	2	507	0.009	0	unknown	2
371	0.010	0	unknown	2	1753	0.009	0	Czech draught	1
372	0.010	0	unknown	2	354	0.008	0	unknown	2
77	0.010	0	unknown	1	709	0.008	0	unknown	2
2123	0.010	0	Noriker	1	355	0.007	0	unknown	2
2129	0.010	0	Noriker	1	784	0.007	0	unknown	2
431	0.010	0	unknown	2	810	0.007	0	unknown	2

*0 = unknown year of birth (until 1930), ** 1 = stallion, 2 = mare

gene contributions come from animals imported from Belgium (Belgian draught horse), 14 % of gene contributions come from local draught horses and 2 % of gene contributions come from Noriker breed. Considering historical development of these breeds, we assume that founders of unknown origin were probably local draught horses, especially if these founders were born until 1930.

The same mare was found as the most genetically contributing founder in both analyzed breeds. Sex ratios in founders explained half of the genetic variation in the reference populations were 35 % of sires and 65 % of dams in Silesian Noriker and 49 % of sires and 51 % of dams in Czech-Moravian Belgian horse respectively. These founder sex ratios were unexpected, because a stallion can produce considerably large number of offspring than a mare. The relatively low effective number of founders reported in both analyzed breeds might explain the relatively high genetic contribution made by the most important founders.

To verify these results, obtained using the pedigree data would be useful further investigation on genomics basis.

4 CONCLUSION

To sum up the foregoing results it could be concluded that values of the effective number of founders and ancestors and founder genome equivalents in relation to the number of founders in Silesian Noriker and Czech-Moravian Belgian populations and the founder contributions to the reference populations indicate loss of genetic variability. The further expected loss of genetic variability in the populations can be minimized by increasing the number of descendants of low-represented founders.

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